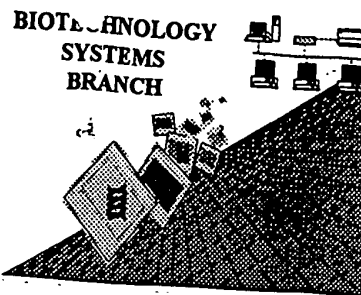


# **RAW SEQUENCE LISTING** **ERROR REPORT**



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/931,457

Source: O/PE

Date Processed by STIC: 8/27/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.  
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:  
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,  
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY  
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.  
PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)  
PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER** **VERSION 3.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

## **Checker Version 3.0**

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25. Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:  
<http://www.uspto.gov/web/offices/pac/checker>

# Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 09/93/487
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 ____ Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 ____ Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 ____ Misaligned Amino Numbering	The numbering under each 5 <sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.	
4 ____ Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 ____ Variable Length	Sequence(s) ____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 ____ PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 ____ Skipped Sequences (OLD RULES)	Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped  Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 ____ Skipped Sequences (NEW RULES)	Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 ____ Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
10 ____ Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence	
11 ____ Use of <220>	Sequence(s) ____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 ____ PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 ____ Misuse of n	n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.	

OIPE

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/931,457

DATE: 08/27/2001

TIME: 13:11:35

Input Set : A:\BB1116 US CIP Seq Listing.txt

Output Set: N:\CRF3\08272001\I931457.raw

Does Not Comply  
Corrected Diskette Needed

3 <110> APPLICANT: Falco, S. Carl  
 4 Allen, Stephen M.  
 6 <120> TITLE OF INVENTION: Plant Amino Acid Biosynthetic Enzymes  
 8 <130> FILE REFERENCE: BB1116 US CIP  
 OK 10 <140> CURRENT APPLICATION NUMBER: US/09/931,457  
 11 <141> CURRENT FILING DATE: 2001-08-16  
 13 <150> PRIOR APPLICATION NUMBER: 09/424,976  
 14 <151> PRIOR FILING DATE: 1998-12-02  
 16 <150> PRIOR APPLICATION NUMBER: 60/065,385  
 17 <151> PRIOR FILING DATE: 1997-11-12  
 19 <150> PRIOR APPLICATION NUMBER: 60/049,406  
 OK 20 <151> PRIOR FILING DATE: 1997-06-12  
 22 <160> NUMBER OF SEQ ID NOS: 72  
 24 <170> SOFTWARE: Microsoft Office 97

## ERRORED SEQUENCES

540 <210> SEQ ID NO: 13  
 541 <211> LENGTH: 306  
 542 <212> TYPE: PRT  
 543 <213> ORGANISM: Oryza sativa  
 545 <400> SEQUENCE: 13  
 546 Leu His Gly Val Phe Val Asn Ile Asp Ser Glu Phe Asp Leu Glu Asn  
 547 1 5 10 15  
 549 Ile Val Thr Ala Ala Arg Val Ala Gly Lys Lys Val Pro Val Leu Leu  
 550 20 25 30  
 552 Arg Ile Asn Pro Asp Val Asp Pro Gln Val His Pro Tyr Val Ala Thr  
 553 35 40 45  
 555 Gly Asn Lys Thr Ser Lys Phe Gly Ile Arg Asn Glu Lys Leu Gln Trp  
 556 50 55 60  
 558 Phe Leu Asp Ser Ile Lys Ser Tyr Ser Asn Asp Ile Thr Leu Val Gly  
 559 65 70 75 80  
 561 Val His Cys His Leu Gly Ser Thr Ile Thr Lys Val Asp Ile Phe Arg  
 562 85 90 95  
 564 Asp Ala Ala Gly Leu Met Val Asn Tyr Val Asp Glu Ile Arg Ala Gln  
 565 100 105 110  
 E--> 567 Gly Phe Glu Leu Glu Tyr Leu Asn Ile Gly Gly Gly Leu Gly Ile (Xaa) see item 9 on  
 568 115 120 125 Even summary  
 570 Tyr His His Thr Asp Ala Val Leu Pro Thr Pro Met Gly Pro His Gln  
 571 130 135 140 sheet  
 573 His Cys Ala Glu Glu Leu Val Leu Ser Arg Asp Leu Thr Leu Ile Ile  
 574 145 150 155 160  
 576 Glu Pro Gly Arg Ser Leu Ile Ala Asn Thr Cys Cys Phe Val Asn Arg  
 577 165 170 175  
 579 Val Thr Gly Val Lys Ser Asn Gly Thr Lys Asn Phe Ile Val Val Asp  
 580 180 185 190

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582 Gly Ser Met Ala Glu Leu Ile Arg Pro Ser Leu Tyr Gly Ala Tyr Gln  
 583 195 200 205  
 585 His Ile Glu Leu Val Ser Pro Ser Pro Asp Ala Glu Val Ala Thr Phe  
 586 210 215 220  
 588 Asp Ile Val Gly Pro Val Cys Glu Ser Ala Asp Phe Leu Gly Lys Asp  
 589 225 230 235 240  
 591 Arg Glu Leu Pro Thr Pro Asp Lys Gly Ala Gly Leu Val Val His Asp  
 592 245 250 255  
 594 Ala Gly Ala Tyr Cys Met Ser Met Ala Ser Thr Tyr Asn Leu Lys Leu  
 595 260 265 270  
 597 Arg Pro Pro Glu Tyr Trp Val Glu Asp Asp Gly Ser Ile Ala Lys Ile  
 598 275 280 285  
 600 Arg Arg Gly Glu Ser Phe Asp Asp Tyr Met Lys Phe Phe Asp Asn Leu  
 601 290 295 300  
 603 Ser Ala  
 604 305

1211 &lt;210&gt; SEQ ID NO: 28

1212 &lt;211&gt; LENGTH: 84

1213 <212> TYPE: DNA PRT

1214 &lt;213&gt; ORGANISM: Triticum aestivum

1216 &lt;400&gt; SEQUENCE: 28

1217 Leu Glu Ser Glu Lys Ala Val Ser Gly Phe His Ala Asp Asn Ile Ala  
 1218 1 5 10 15  
 1220 Pro Ala Ile Leu Gly Gly Phe Val Leu Val Arg Ser Tyr Asp Pro Phe  
 1221 20 25 30  
 1223 His Leu Val Pro Leu Ser Phe Pro Pro Ala Leu Arg Leu His Phe Val  
 1224 35 40 45  
 1226 Leu Val Thr Pro Asp Phe Glu Ala Pro Thr Ser Lys Met Arg Ala Ala  
 1227 50 55 60  
 1229 Leu Pro Arg Gln Val Asp Val Gln Gln His Val Arg Asn Ser Ser Gln  
 1230 65 70 75 80

E- 1232 Ala Ala Ala Leu

3719 &lt;210&gt; SEQ ID NO: 72

3720 &lt;211&gt; LENGTH: 381

3721 &lt;212&gt; TYPE: PRT

3722 &lt;213&gt; ORGANISM: Triticum aestivum

3724 &lt;400&gt; SEQUENCE: 72

E--&gt; 3724 72

W--&gt; 3726 &lt;210&gt; SEQ ID NO:

W--&gt; 3726 &lt;211&gt; LENGTH:

W--&gt; 3726 &lt;212&gt; TYPE:

W--&gt; 3726 &lt;213&gt; ORGANISM:

E--&gt; 3726 &lt;400&gt; SEQUENCE: 2

E--> 3727 His Glu Ser Val Ala Thr Ile Leu Thr Ser Phe Glu Asn Ser Phe Asp  
 3728 1 5 10 15  
 3730 Lys Tyr Gly Ala Leu Ser Thr Pro Leu Tyr Gln Thr Ala Thr Phe Lys  
 3731 20 25 30  
 3733 Gln Pro Ser Ala Thr Val Asn Gly Ala Tyr Asp Tyr Thr Arg Ser Gly  
 3734 35 40 45

## RAW SEQUENCE LISTING

DATE: 08/27/2001

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Input Set : A:\BB1116 US CIP Seq Listing.txt

Output Set: N:\CRF3\08272001\I931457.raw

```

3736 Asn Pro Thr Arg Asp Val Leu Gln Ser Leu Met Ala Lys Leu Glu Lys
3737      50                      55                      60
3739 Ala Asp Gln Ala Phe Cys Phe Thr Ser Gly Met Ala Ser Leu Ala Ala
3740 65                      70                      75                      80
3742 Val Thr His Leu Leu Gln Ala Gly Gln Glu Ile Val Ala Gly Glu Asp
3743                      85                      90                      95
3745 Ile Tyr Gly Gly Ser Asp Arg Leu Leu Ser Gln Val Val Pro Arg Asn
3746                      100                      105                      110
3748 Gly Ile Val Val Lys Arg Val Asp Thr Thr Lys Ile Asn Asp Val Thr
3749                      115                      120                      125
3751 Ala Ala Ile Gly Pro Leu Thr Arg Leu Val Trp Leu Glu Ser Pro Thr
3752                      130                      135                      140
3754 Asn Pro Arg Gln Gln Ile Thr Asp Ile Lys Lys Ile Ser Glu Ile Ala
3755 145                      150                      155                      160
3757 His Ser His Gly Ala Leu Val Leu Val Asp Asn Ser Ile Met Ser Pro
3758                      165                      170                      175
3760 Val Leu Ser Trp Pro Ile Glu Leu Gly Ala Asp Ile Val Met His Ser
3761                      180                      185                      190
3763 Ala Thr Lys Phe Ile Ala Gly His Ser Asp Leu Met Ala Gly Ile Leu
3764                      195                      200                      205
3766 Ala Val Lys Gly Glu Ser Leu Ala Lys Glu Ile Ala Phe Leu Gln Asn
3767                      210                      215                      220
3769 Ala Glu Gly Ser Gly Leu Ala Pro Phe Asp Cys Trp Leu Cys Leu Arg
3770 225                      230                      235                      240
3772 Gly Ile Lys Thr Met Ala Leu Arg Val Glu Lys Gln Gln Asp Asn Ala
3773                      245                      250                      255
3775 Gln Lys Ile Ala Glu Phe Leu Ala Ser His Pro Arg Val Lys Gln Val
3776                      260                      265                      270
3778 Asn Tyr Ala Gly Leu Pro Asp His Pro Gly Arg Ser Leu His Tyr Ser
3779                      275                      280                      285
3781 Gln Ala Lys Gly Ala Gly Ser Val Leu Ser Phe Gln Thr Gly Ser Leu
3782                      290                      295                      300
3784 Ser Leu Ser Lys His Val Val Glu Thr Thr Lys Tyr Phe Asn Val Thr
3785 305                      310                      315                      320
3787 Val Ser Phe Gly Ser Val Lys Ser Leu Ile Ser Leu Pro Cys Phe Met
3788                      325                      330                      335
3790 Ser His Ala Ser Ile Pro Ser Ser Val Arg Glu Glu Arg Gly Leu Thr
3791                      340                      345                      350
3793 Asp Asp Leu Val Arg Ile Ser Val Gly Ile Glu Asp Val Asp Asp Leu
3794                      355                      360                      365
3796 Ile Ala Asp Leu Asp Tyr Ala Leu Arg Ser Gly Pro Ala
3797                      370                      375                      380

```

09/931,457 4

<210> 72  
<211> 381  
<212> PRT  
<213> Triticum aestivum

<400> 72

<400> 2 delete

## VERIFICATION SUMMARY

DATE: 08/27/2001

PATENT APPLICATION: US/09/931,457

TIME: 13:11:36

Input Set : A:\BB1116 US CIP Seq Listing.txt

Output Set: N:\CRF3\08272001\I931457.raw

L:10 M:270 C: Current Application Number differs, Replaced Application Number  
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:216 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:5  
L:216 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:218 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:5  
L:218 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:219 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:5  
L:219 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:220 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:5  
L:220 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5  
L:567 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:13  
L:769 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:16  
L:769 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16  
L:770 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:16  
L:770 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16  
L:771 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:16  
L:771 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16  
L:772 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:16  
L:772 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16  
L:773 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:16  
L:773 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16  
L:774 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:16  
L:774 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16  
L:825 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:18  
L:825 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18  
L:826 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:18  
L:826 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18  
L:846 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:19  
L:846 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19  
L:1014 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:23  
L:1014 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23  
L:1016 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:23  
L:1016 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23  
L:1042 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:24  
L:1042 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24  
L:1206 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:27  
L:1206 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27  
L:1209 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:27  
L:1209 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27  
L:1232 M:252 E: No. of Seq. differs, <211>LENGTH:Input:84 Found:0 SEQ:28  
L:1595 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:35  
L:1595 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:35  
L:1596 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:35  
L:1596 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:35  
L:1597 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:35  
L:1597 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:35  
L:1598 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:35  
L:1598 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:35

## VERIFICATION SUMMARY

PATENT APPLICATION: US/09/931,457

DATE: 08/27/2001

TIME: 13:11:36

Input Set : A:\BB1116 US CIP Seq Listing.txt

Output Set: N:\CRF3\08272001\I931457.raw

L:1599 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:35  
L:1599 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:35  
L:1827 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:39  
L:1827 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:39  
L:1829 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:39  
L:1829 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:39  
L:1830 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:39  
L:1830 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:39  
L:1831 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:39  
L:1831 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:39  
L:1859 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:40  
L:1859 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:40  
L:1865 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:40  
L:1865 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:40  
L:3724 M:252 E: No. of Seq. differs, <211>LENGTH:Input:381 Found:0 SEQ:72  
L:3726 M:282 W: Numeric Field Identifier Missing, <210> is required.  
L:3726 M:282 W: Numeric Field Identifier Missing, <211> is required.  
L:3726 M:282 W: Numeric Field Identifier Missing, <212> is required.  
L:3726 M:282 W: Numeric Field Identifier Missing, <213> is required.  
L:3726 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:72 differs:2  
L:22 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (72) Counted (73)